

10/04/03

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 07:42:58 : Search time 384 Seconds
(without alignments)
16221.425 Million cell updates/sec

Sequence: 1 atggcgcgttaagtgatgca.....gtcatcaaggggtctctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database 8 NGeneseq-10100280

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2766.2	99.8	2762	ABN83428	Human transporter
2	2766.2	98.8	2761	ABN83428	Human transporter
3	1784.8	64.5	126512	ABN83429	Human transporter
4	1326.4	48.0	2814	ABN83429	Human transporter
5	1277.8	46.2	4291	ABN83429	Human transporter
6	1227.8	44.4	4087	ABN83429	Human transporter
7	1208.8	43.7	5438	ABN83429	Human transporter
8	897.4	32.4	1187	ABN83429	Human transporter
9	787.2	28.5	1836	ABN83429	Human transporter

10	787.2	28.5	1836	22	ABN83428	Human transporter
11	787.2	28.5	1836	22	ABN83428	Human transporter
12	787.2	28.5	1836	22	ABN83428	Human transporter
13	787.2	28.5	1836	22	ABN83428	Human transporter
14	787.2	28.5	1836	22	ABN83428	Human transporter
15	593.2	21.4	4546	23	ABN83428	Human transporter
16	363	13.1	363	23	ABN83428	Human transporter
17	319	11.5	24221	23	ABN83428	Human transporter
18	219.4	7.9	381	22	ABN83428	Human transporter
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21	219.4	7.9	381	22	ABN83428	Human transporter
22	219.4	7.9	381	22	ABN83428	Human transporter
23	219.4	7.9	381	22	ABN83428	Human transporter
24	219.4	7.9	381	22	ABN83428	Human transporter
25	219.4	7.9	381	22	ABN83428	Human transporter
26	219.4	7.9	381	22	ABN83428	Human transporter
27	198.8	7.2	458	22	ABN83428	Human transporter
28	198	7.2	325	22	ABN83428	Human transporter
29	186.4	6.7	491	22	ABN83428	Human transporter
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ALIGNMENTS

RESULT 1	ABN83428	standard; cDNA; 2782 BP.
ID	ABN83428	
AC	ABN83428	
DT	21-AUG-2002	(first entry)
DE	Human transporter protein coding sequence.	
KW	Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;	
KW	spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.	
OS	Homo sapiens.	
FT	key	Location/Qualifiers
FT	CDS	10..2775
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FT	FT	/product="Human transporter"
PN	WO200233086-A2.	
PD	25-APR-2002.	
PP	17-OCT-2001; 2001WO-US32152.	
PR	17-OCT-2000; 2000US-240836P.	
PR	13-MAR-2001; 2001US-0804474.	
PA	(PEKE) PE CORP NY.	
PI	Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;	

PI Beasley EM;
XX
XX WPI: 2002-479677/51.
DR P-PSDB: AB883246.
XX
PT Human transporter peptide related to sodium/calcium exchanger subfamily
PT for identifying modulators useful for treating a disease or condition
PT mediated by human transporter protein
XX
XX Claim 4; Fig 1; 200pp; English.
XX
CC The present sequence is the coding sequence of a human transporter
CC protein, which is related to the sodium/calcium exchanger subfamily.
CC Experimental data indicates expression of the transporter gene in humans
CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR.
XX
XX Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 other;
SO

Query Match 99.8%; Score 2761.2; DB 24; Length 2782;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 TTTGTGCTCTTCTCGAATGCTCTCGAGCAGAGCTGTGGCTCAGGGGACGTGCCAAGC 120
DB 70 TTTGTGCTCTTCTCGAATGCTCTCGAGCAGAGCTGTGGCTCAGGGGACGTGCCAAGC 129
QY 121 ACAGGCGAACAATGAGTCTCTTCAGGGTCATCGAGCTGCAAGAGAGGTGTCTATCTG 180
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QY 181 CCAATCTGTAACCCGCGAAGACCTTCCCTTGGGACAAGATTGGCAGGGTCTATCTAT 240
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QY 301 TCTATTGAGTCATCAGCTCTCAAGAGAGGAGTGCAATTAAAGAACCAATGAGAA 360
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QY 481 ATTGCTGAGTATCTGGGACCTTCTACCATTTGAGGAGTGCAGGCTTCAACATGTTATC 540
DB 490 ATTGCTGAGTATCTGGGACCTTCTACCATTTGAGGAGTGCAGGCTTCAACATGTTATC 549
QY 541 ATCATTTGGCATCTGTGCTACGTGATCCAGAGGAGAGACTGCAAGATCAAGCATCTA 600
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DB 730 TTTTCCAGTGTGTCTCTTCTGGGCTGGGTGGAGATTAACGACTGCTCTTCAAAATAC 789
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QY 1801 AAAATAGTACATGAGAGAGATACGAAGGCAAGACAATTTCTTCAATGTGCCCTTGTGAA 1860
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OY 1921 GAGGAGGCCAAGAGATAGCAGATGGGAAGCCAGTATTTGGTGAACACCCAAACTA 1980
DB 1930 GAGGAGGCCAAGAGATAGCAGATGGGAAGCCAGTATTTGGTGAACACCCAAACTG 1989
OY 1981 GAAGTCATCATTTGAAGAGTCTATGAGTTCAAGACTACGGTGACAACTGATCAAGAAG 2040
DB 1990 GAAGTCATCATTTGAAGAGTCTATGAGTTCAAGACTACGGTGACAACTGATCAAGAAG 2049
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DB 2050 ACAAACCTGGGCTTTGGTGGGAGCCCATTCCTGGAGGAGACAGTCAATGAGAGCCATC 2109
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DB 2410 ACCAAAGCTGCGCCCTCCAGATGATATGACAGACGCTCCATGAGGAAAGTGAACGGGAC 2469
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DB 2590 CTCTTCACCATCTTTGATTTGCTGATCAGAGGTGCTCTTGTACCGAAGGGGGCGGAC 2649
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DB 2650 CTGGGAGGGGAGCTTGGTGGCCCCCGCTGCTGACAGCTGCGCAACAACATGGCTTTGTG 2709
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DB 2710 AGCTGTGGCTCTCTCTACATCTCTTTGGCACACTTGAAGGCTTATGCTACATCAAGGGG 2769
OY 2761 TTCTAA 2766
DB 2770 TTCTAA 2775

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RESULT 2
ABAO4756
ID ABAO4756 standard; cDNA; 2781 BP.
XX
AC ABAO4756;
XX
DT 25-FEB-2002 (first entry)

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XX DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.
XX KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
XX KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
XX KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiac; Vaccine;
XX KW coronary heart disease; renal failure; ischemic disorder;
XX KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.
XX OS Homo sapiens.
XX FH Key
XX FH CDS
XX FT Location/Qualifiers
XX FT 1..2781
XX FT /*tag= a
XX FT /partial
XX FT /product= "Human natrium(+)-calcium(2+) exchanger form 3
XX FT protein, HNCX3"
XX FT /note= "No stop codon given"
XX PN MO200183744-A2.
XX PD 08-NOV-2001.
XX PF 30-APR-2001; 2001WO-EP04886.
XX PR 02-MAY-2000; 2000EP-0109080.
XX PA (MERK ) MERCK PATENT GMBH.
XX PI Wilm C;
XX DR MPI: 2002-041493/05.
XX DR P-PSDB: AAM47745.
XX PT New polypeptide, useful as vaccines for inducing immune response
XX PT against diseases such as myocardial infarction, arrhythmia, ischemic
XX PT disorders, renal disorders in mammal -
XX PS Claim 4; Page 34-38; 41pp; English.
XX CC The present sequence is the coding sequence for human Natrium(+)-Calcium
XX CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
XX CC 14. HNCX3 and its coding sequence are useful for treating acute and
XX CC chronic cardiac failure of different aetiologies, myocardial infarction,
XX CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
XX CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
XX CC acute and chronic renal failure, ischemic disorders of skeletal muscle
XX CC and ischaemic brain disorders of different aetiologies.
XX SQ Sequence 2781 BP; 658 A; 678 C; 765 G; 680 T; 0 other:
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XX Query Match 98.8%; Score 2733.4; DB 24; Length 2781;
XX Best Local Similarity 99.3%; Pred. No. 0;
XX Matches 2762; Conservative 0; Mismatches 1; Indels 18; Gaps 1;
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DB 1 ATGGCGGTGATTAAGTTGAGGCTCTACCTGCTTCTCCATTTTGGGCTGTTACC 60
OY 61 TTTGTCTCTTCTCCTGAATGTTTTCGAGCAGAGGCTGTGGCTCAGAGGAGCTGCACAC 120
DB 61 TTTGTCTCTTCTCCTGAATGTTTTCGAGCAGAGGCTGTGGCTCAGAGGAGCTGCACAC 120
OY 121 ACAGGGCAGACAAAGTATGCTGTTTCAGGCTCATGCGACTGCAAGAGGCTGTCATCTTG 180
DB 121 ACAGGGCAGACAAAGTATGCTGTTTCAGGCTCATGCGACTGCAAGAGGCTGTCATCTTG 180
OY 181 CCAATCTGTACCCGAGAGACCTTCCCTTGGGAGCAAGATTGGCCAGGGTCAATGCTATP 240
DB 181 CCAATCTGTACCCGAGAGACCTTCCCTTGGGAGCAAGATTGGCCAGGGTCAATGCTATP 240
OY 241 TTTGTGGCCCTGATATACATGTTCTTGGGAGTCCATGCTGACCGCTTCATGGCA 300
DB 241 TTTGTGGCCCTGATATACATGTTCTTGGGAGTCCATGCTGACCGCTTCATGGCA 300

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Db 241 TTGTGGCCCTGAAATACATGTTCCCTGGGGTGTCCATCATGTCGTGACCGCTTCATGCA 300
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Db 361 ACAGACACACACATATTGCGGCTGGAATGAACATGTCCTCAACCTGACCTTATGAGCC 420
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QY 1561 GTTACCATCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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Db 1621 GTCAAGAGAGATATTGTTATGAGGTCAAGGTTCTGCGACATCAGGTGCGGAGGT 1680
QY 1681 ACAGTCAATCCCTCCCTTAAAGACATGAAAGGACACCAAGGCTGGCGGTGAGACTTT 1740
Db 1681 ACAGTCAATCCCTCCCTTAAAGACATGAAAGGACACCAAGGCTGGCGGTGAGACTTT 1740
QY 1741 GAAACACATATTGGGAGATTGGAATTCAGAAATGATGATGATGATGATGATGATGATGAT 1800
Db 1741 GAAACACATATTGGGAGATTGGAATTCAGAAATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 AAAATAGTATGAGAGAGAAATACGAAAGGACAGAGAAATTTCTTATGCTCCCTTGTGAA 1860
Db 1801 AAAATAGTATGAGAGAGAAATACGAAAGGACAGAGAAATTTCTTATGCTCCCTTGTGAA 1860
QY 1861 CCGAAATGATGAGAACTGGAATATC-----AGATGTGACAGAGAG 1920
Db 1861 CCGAAATGATGAGAACTGGAATATC-----AGATGTGACAGAGAG 1920
QY 1903 AAGCTGACTATGAGAAAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 1962
Db 1903 AAGCTGACTATGAGAAAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 1962
QY 1921 AAGCTGACTATGAGAAAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 AAGCTGACTATGAGAAAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 1980
QY 1963 GGTGACACCCCAAACTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2022
Db 1963 GGTGACACCCCAAACTAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2022
QY 2023 GACAACTGATCAAGAGAAACCTGCGCTTGTGAGGAGCCATTCCTGAGAGGAC 2082
Db 2041 GACAACTGATCAAGAGAAACCTGCGCTTGTGAGGAGCCATTCCTGAGAGGAC 2100
QY 2083 CAGTTCAATGAGAGCCATCACCGTCACTGACAGAGAGAGATGATGATGATGATGATGATGAT 2142
Db 2101 CAGTTCAATGAGAGCCATCACCGTCACTGACAGAGAGAGATGATGATGATGATGATGATGAT 2160
QY 2143 GAGGAGAGCGTCCCTCTGCTTGTGACTAGCTATGATGATGATGATGATGATGATGATGAT 2202
Db 2161 GAGGAGAGCGTCCCTCTGCTTGTGACTAGCTATGATGATGATGATGATGATGATGATGAT 2220
QY 2203 GTGCTGTTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2262
Db 2221 GTGCTGTTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
QY 2263 TCCATCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2322
Db 2281 TCCATCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
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Db 2341 TGACCAATGTTGCTCAAAAGATTCAGTCACAGCTGTTTCTGTTGCTGTTGCTGCTGCTGCT 2400
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OY 2443 ATTGCAACGTACAGGGGACGACCAACGCCGTCAATGTCCTCTGGGCAATCGGCGCTGCGCTGG 2502
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OY 2503 TCCGTGGCGCCGATCATACAGGGGCTCGAGGGGACAGAGATTCACAGTTCGCGCGGCGACCA 2562
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DB 2581 CTGGGCTTCCTCGGTACACCTCTTTCACACATCTTTCGATTCGATCAGCGGTGCTCTTG 2640
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DB 2641 TACCGAAGCGCGCCGACCTGGAGGGGAGCTTGGTGCCGCCGCTGGCAAGCTCGCC 2700
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DB 2701 ACACATGGCTCTTGTGAGCCGTGGGCTCTCTACATCTCTTTCGACACAGAGAGGCC 2760
OY 2743 TATTGCTACATCAAGGGGTTTC 2763
DB 2761 TATTGCTACATCAAGGGGTTTC 2781

RESULT 3
ABN83429
ID ABN83429 standard; DNA; 126512 BP.
XX
AC ABN83429;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human transporter protein gene.
XX
KM Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KM spleen; testis; leukocyte; foetal brain; chromosome 14; gene;
KW single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key
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Best Local Similarity 99.9%: Pred. No. 0:
Matches 1786: Conservative 0: Mismatches 2: Indels 0: Gaps 0:
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DB 2010 ATGGCGTGTAAAGTTGACGCTCTCACCCTCTCCCTTCATTTTGGCGTGTACC 2069
QY 61 TTTGTGCTCTTCGTAATGCTCTTCGAGCAGAGCTGTGGCTCAGGGAGCTGCCAAGC 120
DB 2070 TTTGTGCTCTTCGTAATGCTCTTCGAGCAGAGCTGTGGCTCAGGGAGCTGCCAAGC 2129
QY 121 ACAGGGAGAAACATAGATGCTCTTCAGGGTCATCGGACATGCAAGAGGGTGCATCTG 180
DB 2130 ACAGGGAGAAACATAGATGCTCTTCAGGGTCATCGGACATGCAAGAGGGTGCATCTG 2189
QY 181 CCAATCTGTACCCGAGAACCTTCCCTTGGGACAAAGATTGCCAGGGTCATTGTCTAT 240
DB 2190 CCAATCTGTACCCGAGAACCTTCCCTTGGGACAAAGATTGCCAGGGTCATTGTCTAT 2249
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QY 421 CTGGGTCCTCTGCTCTCGAGATACTCTCTCTTTAATTAGAGTGTGGTCATGGGCTC 480
DB 2430 CTGGGTCCTCTGCTCTCGAGATACTCTCTCTTTAATTAGAGTGTGGTCATGGGCTC 2489
QY 481 ATTGCTGTGATCTGGGACCTTCTACCAATTGTAGGAGTGAAGCTTCAACATGTTCATC 540
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DB 2550 ATCATTTGGCATCTGTGCTTACGTGATCCAGACGAGAGACTCGCAAGATCAACATCTA 2609
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DB 2610 CGAGTCTTCTCATCACCGCTGCTTGGAGATCTTTTGGCTTACATCTGCTTATATGAT 2669
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DB 2670 CTGGCAGTCTTCTCCCTGCTGAGTGTGTCAGGTTTGGGAAGGCTCTCACTCTTCTTTC 2729
QY 721 TTTTCAGTGTGCTGCTTCTTGGCCCTGGGTGGCAGATAAACAGCTGCTTCTTACAAATAC 780
DB 2730 TTTTCAGTGTGCTGCTTCTTGGCCCTGGGTGGCAGATAAACAGCTGCTTCTTACAAATAC 2789
QY 781 ATGCACAAAAGTACCGCAGACAGAACACCGAGAGATTATCATAGACAGAGGGTGAC 840
DB 2790 ATGCACAAAAGTACCGCAGACAGAACACCGAGAGATTATCATAGACAGAGGGTGAC 2849
QY 841 CACCTTAAGGCATTTGATGATGATGGGAAATGATGATCCCTTTTCTAGATGGGAC 900
DB 2850 CACCTTAAGGCATTTGATGATGATGGGAAATGATGATCCCTTTTCTAGATGGGAC 2909

Oy	901	CTGTGTCCTCCGTAAGGAAAGAAAGTGAATGATCCGCCAGAGAGATATCCGATATCTC	960
Db	2910	CTGTGTCCCTCGTAAGGAAAGAAAGTGAATGATCCGCCAGAGATATATCCGATATCTC	2969
Oy	961	AAGGATCTGAAGCAAAAACACCAGAGAGACTTATAGATACACTGGTGAATGGCCAT	1020
Db	2970	AAGGATCTGAAGCAAAAACACCAGAGAGACTTATAGATACACTGGTGAATGGCCAT	3029
Oy	1081	ATGATGACTGTCGTCAGAGCAATATCTCGAAGAAACATGCAGCAAGAACCCAAAGGCC	1140
Db	3090	ATGATGACTGTCGTCAGAGCAATATCTCGAAGAAACATGCAGCAAGAACCCAAAGAGCC	3149
Oy	1141	TCCAGCATGATGACGAGGTGCGACACCGATGAGCCTGAGAGACTTATATTCGAAGCTCTCTT	1200
Db	3150	TCCAGCATGATGACGAGGTGCGACACCGATGAGCCTGAGAGACTTATATTCGAAGCTCTCTT	3209
Oy	1201	GACCCATGTTCTTACCAAGTCGCCGTGGAGAACTGTGGGGCTGTACTCTGACAGTGTGAGG	1260
Db	3210	GACCCATGTTCTTACCAAGTCGCCGTGGAGAACTGTGGGGCTGTACTCTGACAGTGTGAGG	3269
Oy	1261	AAAGGGGGAGACATGTCGAAAGACCATGATGTGGTACTACAAAACAGAGATGTTCTCC	1320
Db	3270	AAAGGGGGAGACATGTCGAAAGACCATGATGTGGTACTACAAAACAGAGATGTTCTCTCC	3329
Oy	1321	AATGACAGGGGCTACTATGATGTTCAAGAGGGGACGGTGCTGTACACCCAGAGAGAGCC	1380
Db	3330	AATGACAGGGGCTACTATGATGTTCAAGAGGGGACGGTGCTGTACACCCAGAGAGAGCC	3389
Oy	1381	CAGAGAGAGTTCTCCGTGGGCAATATTTGATGACAGCAATTTTGGAGAGATGAACACTTC	1440
Db	3390	CAGAGAGAGTTCTCCGTGGGCAATATTTGATGACAGCAATTTTGGAGAGATGAACACTTC	3449
Oy	1441	TTTGTAAAGTTGAGCAATGTCCGATAGAGAGAGAGACCCAGAGAGGGATGCTTCCA	1500
Db	3450	TTTGTAAAGTTGAGCAATGTCCGATAGAGAGAGAGACCCAGAGAGGGATGCTTCCA	3509
Oy	1501	GCAATATTCAAAGTCTCCCTTGCCCTGGGGCGTCCTAGCCTCCCTTGTGTGGCCACA	1560
Db	3510	GCAATATTCAAAGTCTCCCTTGCCCTGGGGCGTCCTAGCCTCCCTTGTGTGGCCACA	3569
Oy	1561	GTTTACCATCTTGATGATGACCAATGCAGGCACTTCTACTTTGAATGTGATACTATTCAT	1620
Db	3570	GTTTACCATCTTGATGATGACCAATGCAGGCACTTCTACTTTGAATGTGATACTATTCAT	3629
Oy	1621	GTCAGTGAGAGTATTTGGTATTATGAGAGTCAAGGTTCTGCGGACATCAGGTGCCGGGGT	1680
Db	3630	GTCAGTGAGAGTATTTGGTATTATGAGAGTCAAGGTTCTGCGGACATCAGGTGCCGGGGT	3689
Oy	1681	ACACTACTGCTCCCTTTAGGACAGTAAAGGAGACCAAGGTTGGGGGTGAGGACATTT	1740
Db	3690	ACACTACTGCTCCCTTTAGGACAGTAAAGGAGACCAAGGTTGGGGGTGAGGACATTT	3749
Oy	1741	GAAGACACATATGGGAGTGTGAATTCAGAAATGATGAATCTGTGAAA 1788	
Db	3750	GAAGACACATATGGGAGTGTGAATTCAGAAATGATGAATCTGTGAAA 3797	
RESULT 4			
AAH57377			
ID ID AAH57377 standard; cdna: 2814 BP.			
XX AAH57377:			
XX 10-SEP-2001 (first entry)			
DE Human heart cell specific cdna sequence SEQ ID NO:217.			
XX Human: tissue specific: diagnosis; brain; heart; skeletal muscle;			
KW lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;			

[illegible]

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OY 529 AACATGTTTCATCATTTGGATGCTGTGTAGAGTCCAGACGGAGACACGCAAG 588
Db 532 AATATGTTTCATCATTTATGACCTGCTGTGTATGTGTGTGCTGACGGAGACAAAGAG 591
OY 589 ATCAAGCATCTACGAGCTCTCTTCATCAGCCGCTTGAGATATCTTTGCTACATCTG 648
Db 592 ATTAAGCATTTGGCGTCTCTTGTGTGACAGACCTGAGACATCTTTGCCATACCTCG 651
OY 649 CTCATATGATTTGCGAGCTCTTCCCTGCTGTGTGCTGAGGTTGGGAAGCCCTCTC 708
Db 652 CTTCATATTAATTTGTGTGTGCTATCTCTGCTGTGTGAGGCTGTGGGAAGTTGCTT 711
OY 709 ACTCTCTCTCTCTTCCAGTGTGTGCTGCTGTGCTGGGAGGAGATTAACGACTGTC 768
Db 712 ACTTCTCTCTCTCTTCCCATCTGTGTGTGTGCTGCTGGGAGGATAGGAGACTTCTG 771
OY 769 TTCTACAAATACATGACACAAAAGTACCGACAGACAAACCCGAGAAATATCATAGAG 828
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OY 880 TCCCATTTTCTAGATGGGAACCTGTGCCCCCTGGAGGGAAG----- 921
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OY 1879 GGAATATCAG-----ATGTGACAGACAGAGAACTGACTATG 1914
Db 1903 GGAATGAAGAGTGGCTTACAAATTAACAGACGAATATGATGCAAGCAGCACTGACAGC 1962
OY 1915 GAAGAAAGAGAGCGCAAGAGATGACAGAGATGGGAAGACCACTGATTTGGTGAACACCC 1974
Db 1963 AANAGGAAGAGAGAGAGCGCATTTGCAAAATGGGGGCCCCACCTCCGGAGAGACACACC 2022
OY 1975 AAATGAGATCATATTGAAGAGTCCGTATGATGTTCAAGACTACGTTGACAAACATGATC 2034
Db 2023 AAGTTGGAAGGATCATTTGAAGAAATCCATGAATTTCAAGAGTACTGTGCAACAACTATT 2082
OY 2035 AAGAGCAAAACCTGGGCTGTGTGGGGACCCATTCCTGAGGAGGACCAATTCATGAG 2094
Db 2083 AAGAGCAAAACCTGGGCTGTGTGGGGACCTTAACAGCTGGAAGAAACGTTTATTGAA 2142
OY 2095 GCCATACCCGTCAGTGCAGCAGGAGGATGAGATGAGATGATCCGGGAGAGAGGCTG 2154
Db 2143 GCTATCACTGACAGTGTGTGGGAGATGATGACAGCATGAATGTGGGAAGAAACCTG 2202
OY 2155 CCTCTGCTTTTGAATAGTACACTTCCGTGACTGTCTTGTGAAGGTGTGTGCTTGGCC 2214
Db 2203 CCTCTGCTTTTGAATAGTACACTTCCGTGACTGTCTTGTGAAGGTGTGTGCTTGGCC 2262
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Db	2743	TTTGTGCTCCGATATGCGCTTGTACATTTTCTTCCTTCCTCGAGGCGCTACTGCGACATA	2802
QY	2755	AAGGGGTCTTAA	2766
Db	2803	AAAGGCTTCTAA	2814
RESULT 5			
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ID	AAC75706	standard; cdna; 4291 BP.	
XX	AAC75706;		
DT	08-FEB-2001	(first entry)	
DE	Human OREF ORF1261 polynucleotide sequence SEQ ID NO:2521.		
KW	Human: open reading frame; OREF; detection; cytostatic; hepatotropic;		
KW	vulnerable; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;		
KW	anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;		
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;		
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;		
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;		
KW	antianaemic; gene therapy; cancer; proliferative disorder; hypertension;		
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;		
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;		
KW	cholesterol ester storage; systemic lupus erythematosus; infection;		
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;		
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;		
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;		
KW	thrombosis; contraceptive; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200058473-A2.		
XX			
PD	05-OCT-2000.		
XX			
PF	31-MAR-2000; 2000WO-US08621.		
XX			
PR	31-MAR-1999; 99US-0127607.		
PR	02-APR-1999; 99US-0127636.		
PR	05-APR-1999; 99US-0127728.		
PR	30-MAR-2000; 2000US-0540763.		
XX			
PA	(CURA-) CURAGEN CORP.		
XX			
PI	Shimkets RA, Leach M;		
XX			
DR	WPI: 2000-602362/57.		
DR	P-PSDB: AAB41497.		
PT	Novel nucleic acids and peptides derived from open reading frame X,		
PT	useful for treating e.g. cancers, proliferative disorders,		
PT	neurodegenerative disorders and cardiovascular disease -		
XX			
PS	Claim 5; Page 1807-1809; 5507pp; English.		
XX			
CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB4397,		
CC	which represent the human OREF open reading frames 1 to 3161. The OREF		
CC	sequences have activities such as: cytostatic; hepatotropic; vulnerary;		
CC	antipsoriatic; antiparkinsonian; nootropic; neuroprotective;		
CC	osteopathic; anticonvulsant; antiarthritic; immunosuppressant;		
CC	immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;		
CC	antidiabetic; hypotensive; dermatological; immunosuppressive;		
CC	antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;		

CC	antithyroid; and antinaeamic. The sequences can be used for determining
CC	the presence of or predisposition to, or preventing or treating
CC	pathological conditions associated with an OREF-associated disorder. The
CC	nucleic acids can be used to express OREF proteins in gene therapy
CC	vectors. The proteins and nucleic acids may be used to treat cancers,
CC	proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC	graft vs host disease, cardiovascular disease, diabetes mellitus,
CC	hyperextension, hypothyroidism, cholesterol ester storage, systemic lupus
CC	erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC	bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC	allergies, aplastic anemia, burns, wounds, bone and cartilage damage,
CC	nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC	coagulation; to inhibit thrombosis; and as a contraceptive.
CC	
XX	
SQ	Sequence 4291 BP; 745 A; 1405 C; 1301 G; 840 T; 0 other;
	Query Match 46.2%; Score 1277; DB 21; Length 4291;
	Best Local Similarity 69.1%; Pred. No. 0; Mismatches 775; Indels 51; Gaps 5
	Matches 1843; Conservative 0;
QY	130 AACATGAGTCTCTGTTACAGGTCATCGACTGCACAGAGGCGTGCATCTGCCAATCTGG 189
DB	208 AGCACAGGGGGGTGGCAGAGGGTCTTACCGGTGCCACGCGGGGTGCTGTCGCCGCTGG 267
QY	190 TACCCGGAGAACCTTCCTCCCTGGGACAAGATTGCCAGGGTATTGTCTATTTTGTGGCC 249
DB	268 GAGCCCGAGACGACCTCGCTGGGTGACAAAGCGGACGCGAGTGGTACTTTGTGGCC 327
QY	250 CTGATATACATGTCCTTGGGTGGGTGCCATTCATTTGCTGACCGCTTCATGGCATCTATTGA 309
DB	328 ATGGCTACTATGTTCTGGAGTGTCCATCATCGCGACCGTTCATGGCGGCATCGAG 387
QY	310 GTCATCACCTCTCAAGAGAGGAGGTGCACATTAAGAAACCCCAATGAGAAACCAACACA 369
DB	388 GTCATCAGTCAAAAGAGAGAGAGATCAACCATACCAAGGCCAACGGTGTAGACACAGCTG 447
QY	370 ACCACTATTTCGGGTCTGGATGAATAAAGTCTTCAACCTGACCCCTTATGGCCCTGGTTC 429
DB	448 GGCACCTTTCCGATCTGGATGAGACGGGTCCAACCTCACCTCATGGCCCTGGGGCTC 507
QY	430 TCTGCTCGAGATACCTCTCTTAAATGAGGTGTGGTCAATGGGTTCATTTGCTGCT 489
DB	508 TCCGACCTCGAATCTCTGCTGTCACTCATCGAAGTCTGGGGCACAACTTCACAGCGGGT 567
QY	490 GATCTGGGACCTCTTACCACTTTAGAGAGTGGAGCGCTCAACATGCTTCATCATTTGGC 549
DB	568 GAGCTGGGGCCACGACCATCTGGGGCAGCGCTGCTTCAATATGTTTGTGTATCCGCC 627
QY	550 ATCTGTGTACGTATCCAGAGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTC 609
DB	628 GTGTCACTATCGTATCATCCAGCGGAGCGGCAAGATCAAGCACTGAGAGTCTTC 687
QY	610 TTCAATCACCGCTGCTGGAGTATCTTTGGCTTACATCTGGCTTATATGATTTCTGGCAGTC 669
DB	688 TTTGTCACTGCTCTTGGAGCATCTTCGGCTTATGCTGTGCTTATCTCATCTTGGCTGT 747
QY	670 TTCTCCCGGTGTGATGCCAGTTTGGAGAGCGCTTCACCTCTCTCTTCCAGAG 729
DB	748 TTTTCCCGGCTGTGTGATCGAGTGTGGAGGCGGCTGTGACCTGTCTTCTTCCGGTGG 807
QY	720 TGTGTCTTCTTGGCGGTGGGTCACATTAACACACTGCTCTTCTACAAATATATGCACAA 789
DB	808 TGCGTGTGATATGCTGGATGGCCGACAAAGGGGTGCTTCTTACAAAGTATGTATCAAG 867
QY	790 AAGTACCGCACAGACAAACACCGAGGATTTATCATATAGACAGAGGGTGTACCACTTAAG 849
DB	868 CGCTACCGACAGCACCCAGCGGAGCATCATATAGGCGCCGAGGGGACCCCGGAAAG 927
QY	850 GGCATTGGAGTGGAGGAAATGATGGAATTCCTCATTTTCTGTAGTGGGA----- 899
DB	928 AGCATAGAGATGGAGGACGCTTCTGTGGCGCGAGGCCCAAGGTAGCTGGGCGGCTGG 987
QY	900 --CTGTGTGCCCTGGAAGGGAAGATGTGATGATCCCGAGAGATGATCCGATT 957

Db	988	GGCCCCGGGGCCCCGGGGCCGGAGCTGGAGCCCAAGCCCGCGAGGTATCCAGTTC	1047
QY	958	CTCAAGGATCTGAGCAAAAACCCAGAGAGACTTAGATTCAGTGGTGGAGATGGCC	1017
Db	1048	CTCAAGGACCTCAAGCAAGAGACCAGGACAAAGGATCTGGAGCAGTGGTGGGATGCC	1107
QY	1018	AATTACTATGCTCTTTCCCAACAAAGAGAGCCGGCTCTTACCGTATCCAAAGCACT	1077
Db	1108	AACACTACGCGCTGCTGACACAGAGAGCCGCGCTTCTACCGCATCAGAGCCACG	1167
QY	1078	CGTATGATGACTGGTGGAGGCAATATCTGTAGAGAAACATGAGAGAAACAGCAAG	1137
Db	1168	CGGCTGATGACGGCGCGGAGACGTCTGGCAGACACGGCGAGCGCTCGCGAGG	1227
QY	1138	GCCCTCAGCATGAGCAGGTGCACACCGATGAGCCTTATTTCCAAAGCTTTC	1197
Db	1228	GGGGC---GGCGGCGAGAGGGGGGGGAGAGACAGACAGGCGGCGGCGCATCTTC	1284
QY	1198	TTTGACCAATGTTCTTACCACTGCTGAGAACTGTGGGGCTGTACTCTGACAGTGGT	1257
Db	1285	TTTCAGGCTTACGCTCTTACACTGCTGGAGAACTGCGGCTCCGCTGCTCTCCGTACG	1344
QY	1258	AGGAAAGGGGAGACATGTCAAAGACATGTATGTGACTTCAAAACAGAGAGTGTCT	1317
Db	1345	TGCCAGGGCGGAGGAGCAACAGCACCCTTACGTGACTACGCGACTGAGAGCGGCTCT	1404
QY	1318	GCCAAATCAGAGGGGCTGACTATGATTCACAGAGGCAAGGTGTCTTGAAGCCAGAG	1377
Db	1405	GCCAAAGCGGGCTCCGACTACGAGTACAGCAGAGGACGCTGCTTCAACACAGGGAG	1464
QY	1378	ACCCAGAGAGGATCTCCGTGGGCAATATGATGACACATTTTGGAGAGGATGAACAC	1437
Db	1465	ACGCAAGAGAGATCGGATCGCATGATCAGCAGCAGCATCTTCGAGAGAGACAT	1524
QY	1438	TTCTTTTAAAGCTTGACCAATGTCCGATGATGAGAGGAGGCCAGAGAGGGGATGCT	1497
Db	1525	TTCTTCTGTCGGCTGTGAACCTGCGGTGGGCGAGCGGCAATGTTTCAGACCG---	1581
QY	1498	CCAGCAATATTCACACACTTCTCCCTTGGCTGGGCTGTCTGAGCCCTCTTGTGGCC	1557
Db	1582	-----GACGG	1639
QY	1558	ACAGTATACATCTTGGATGATGATGACCATGACAGGACATCTTCACTTTGAATGTATAT	1617
Db	1630	ACCGTACACATCTTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1689
QY	1618	CATGCTAGTAGAGATTTGTTGTTATGGAGGTCAAGGTTGGGGACATACAGTGGCCGG	1677
Db	1690	CACGTGAGCGAGTGCATGAGGACACCGTGCAGCTGCGGTGCGCACCTCGGGGCGCGC	1749
QY	1678	GGTACAGTCACTGCTCCCTTTAGAGCAGTAGAGGAGACAGCCAGGGTGGCGGTGAGAC	1737
Db	1750	GGCAGCGTGGCGCTTCCCTACCGCAGCGTGGAGCGGACGCGCGCGCGGGGGGTGCAC	1809
QY	1738	TTTGAAGACACATATGGGGAGTGGAAATTCAGATGATGAAACTGTGAATCAATAGG	1797
Db	1810	TACGAGGACCGGTGCGGAGAGCTGTGGCTGGCAGCAGCAGCAGCAGCAGCAGCAGC	1869
QY	1798	GTTAAATATGATGATGAGAGGAATAGCAAAAGGCAAGGAATTTCTTCAATTTGCCCTGGT	1857
Db	1870	GTCAGATATGTTGATGACGAGGAATATGAGAAAAAGGATAATTTCTTCAATTTAGCTGGGC	1929
QY	1858	GAACCGAATGATGATGAACTGTGAATATCAGATGTGAC-----GAC	1899
Db	1930	CAGCCCCAGTGGCTTAAGCAGAGGATTTTCACTCTGCTACTCAATCAAGGGATGGGGAC	1989
QY	1900	AGGAAGCTGACTATGAGAGAGAGAGAGGCCAAGAGATAGCAGAGATGGAGAAACCGATA	1959
Db	1990	AGGAAGCTTAACAGCGCAGAGAGAGAGAGGCTCGAGGATAGCAGAGATGGGCAAGCCAGTT	2049
QY	1960	TTGGGTGAACACCCCAACTAGAAATCATATTGATGAGATCTTATGATTTCAAGACTACG	2019
Db	2050	CTTGGGAGAACTCCGGCTGGAGGTCATCATGAGAGATCATATGATTTTAAGAACAGC	2109
QY	2020	GTGACAAACTGATCAAGAAAGAACAACTGGCTTGGTGTGGGAGACCAATCTCTGGAG	2079
Db	2110	GTGATTAAGTATCATCAAGAAAGAACTGGCTTGGTAAATGGGACCAATTCATGAGG	2169
QY	2080	GACCAATTCATGAGGCGCATACCGCTGATGAGC---AGGGATGAGGATGAGGATGAA	2136
Db	2170	GAGCAGTTTATGAGGCAATTAACGTGAGGCGCAGGGAGCAGGAGAGAGAGAGAGCGG	2229
QY	2137	TCCGGGGAGAGAGAGGCTGCGCTCTGCTTGTGATGATGATGATGATGATGATGATG	2196
Db	2230	TCCGGGAGAGAGGCGCTGCGCTGCTGCTTGTGATGATGATGATGATGATGATGATG	2289
QY	2197	TGGAAGTGTCTTGGCTGTGTGCCCCCAGAGAGTACTGCCAGGCTGGGCTGCTTC	2256
Db	2290	TGGAAGTGTCTTGGCTGTGTGCCCCCAGAGAGTACTGCCAGGCTGGGCTGCTTC	2349
QY	2257	GCGCTTCATCTCATCATTTGGCATGCTCACCGCATCATTTGGGAGCTGGCTCGCAC	2316
Db	2350	GGTGTTCATCTCATCATTTGGCATGCTCACCGCATCATTTGGGAGCTGGCTCGCAC	2409
QY	2317	TTGGGCTGACATTTGCTCAAGATTCAGTCAAGCTGCTGTTTCTGGGCAATTGGC	2376
Db	2410	TTGGGCTGACCGTTGGCTCAAGACTGTGATGATGATGATGATGATGATGATGATG	2469
QY	2377	ACCTGTGCCAGATACGTTTCCAGCAAAAGCTGCTGCCCTCCAGAGATGATAGCAGAC	2436
Db	2470	ACCTGTCCCTGTGACAGTTTCCAGCAAAAGGCGGCGCTCCAGAGCAGTGGCCGAC	2529
QY	2437	GCTTCATTTGGCAAGTGCAGGCGGAGCAGACGCCGCTCAATGCTTCTGGGATGCGCTG	2496
Db	2530	GCGTTCATGAGGCAAGCTGACCGGCTCCAGCGGCTGAACGTGTTCTTGGGCTGGGCTC	2589
QY	2497	GCGTGTGCTGCGGCGGCTCACTGAGGCTGAGAGGAGAGGATGCTCAGGTGCGGCC	2556
Db	2590	GCGTGTGCTGCGGCGGCTCACTGAGGCTGAGAGGAGAGGATGCTCAGGTGCGGCC	2649
QY	2557	GGCAGCTGCGCTTCTCCGTCACCCCTTTCACATCTTTCATTTGCTCATCAGCGTG	2616
Db	2650	GGCAGCTGCGCTTCTCCGTCACCGCTTTCACCGTCTTCCGCTTGTGGGATGCCGTG	2709
QY	2617	CTCTTATACGAAAGCGGCGGCACTGAGAGAGGAGGAGCTTGGTGGCGCCGTGGCAAG	2676
Db	2710	CTGCTGTACCGGCGGCGGCGGACATCGGCGGCGAGCTGGGCGGCGGCGGAGCCAG	2769
QY	2677	CTGCGCAACATGAGCTTGTGAGGCTGAGGCTGCTCAATACATCTTTCAGACACTA	2736
Db	2770	CTGCGCAACATGAGCTTGTGAGGCTGAGGCTGAGGCTGCTCAATACATCTTTCAG	2829
QY	2737	GAGGCTTATGCTTACATCAAGGGGTTCTA	2765
Db	2830	GAGGCTTATGCTTACATCAAGGGGTTCTA	2858
RESULT 6			
AAD24450			
ID	AAD24450 standard; cDNA; 4087 BP.		
AAD24450:			
AC	AAD24450:		
XX			
DT	07-MAY-2002 (first entry)		
XX			
DE	Bovine NCX-1 cDNA.		
XX			
KW	Bovine; recombinant protein; larvae expression system; membrane protein;		
KW	transport protein; cardiac sodium-calcium exchange protein; Na-K ATPase;		
KW	NCX1; cystic fibrosis transmembrane conductance regulator; CFTR; vaccine;		
KW	channel forming protein; junctional protein; connexin 32; ss.		
OS	Bos taurus.		
XX			
FH	Key		
Location/Qualifiers			

D 1747 AACGTCAAAGTATCTTTGGAACCTCGAAGACGGCATCTCGAAGC-----CAGT 1797
OY 1516 CTTCCCTTGGCTCGGGCTGTCTAGACCTCCCTTGTGTGGACACAGTTACCATCTTGAT 1575
D 1798 CATCTCTCAACCTTGGCTGGATGCCCTCCACTGCAACCGGACATTTTGGAT 1857
OY 1576 GATGACCATGAGGACATCTTCTACTTTGAAATGTGATACTATTCATGTGACAGATATT 1635
D 1858 GATGACCATGAGGACATCTTCTACTTTGAAATGTGATACTATTCATGTGACAGATATT 1917
OY 1636 GGTGTATGAGGTCAAGTGTCTGCGGACATCAAGTGGCCGGGTACAGTACCTGCTCCC 1695
D 1918 GGCATCTGAGAGTGAAGTCTGAGAACATCTGGAGCAGGTGGAATGTTATCTGCC 1977
OY 1696 TTTAGACAGTAGAAGGACAGCCAGAGGTGGCGGTGAGACTTTTGAAGACATATGGG 1755
D 1978 TATTAAGACATTTAGGGGACCGCCAGAGGTGAGGGGAGACTTTGAGACACATGGGA 2037
OY 1756 GAGTGGATTTCAAGATGATGAAGTGTGAAAACCATTAAGGCTTAAATAGTAGATAG 1815
D 2038 GAGTCCAGATTCCAGATGAGCAAAATGTCAAAACATATCAGTCAAGTAAATGATGAT 2097
Y 1816 GAGGAATAGCAAGGCAAGAAATTTCTCATTTGCCCTGTGAACCGAATGATGG-- 1873
D 2098 GAGGAGTATGAGAAACAAAGACCTTCTCTTGTGAGATTGAGAGCCCGCTGGTGAG 2157
OY 1874 -----AACGTGAA 1882
D 2158 ATGAGTAGAAGAAAGCCCTGTTATTGATGAGCTTGGCTTCAACATTAACAGGAAA 2217
OY 1883 TATCAGATGTGACAGACAG----- 1901
D 2218 TACCTGTATGGCCAGCGCTGTTCAGAGAAATTCTACTGAGAACATCCACTCCCTCT 2277
OY 1902 -----GAAAGTACTATGAAAGAG 1923
D 2278 ACTATATCAACCATCCGAGATGAATATGATGACAGACGACCTGACACAAAGAGAG 2337
OY 1924 GAGGCCAAGAGATAGCAGATGAGGAAGCCAGTATTTGGTGAACACCCCAACTAGAA 1983
D 2338 GAAGAGAGGCGCATTTGGGAAATGGGGCCCATTTCTGGAGAGCAGACAGACTGGAG 2397
OY 1984 GTGATCATTTGAAGAGTCTTATGAGTTCAGACTACAGTGGTGAACAACTGATCAAGAGACA 2043
D 2398 GTGATCATTTGAAGAGTCTTATGAGTTCAGACTACAGTGGTGAACAACTGATTAAGAGACA 2457
OY 2044 AACCTGGCCCTTGGTGGGGACCCATTCCTGGAGGAGACATTCATGGAGGACATCAC 2103
D 2458 AACCTAGCCCTCTGTTGGGACGAACAGCTGGAGAGACAGTTTCATCGAGGATCACT 2517
OY 2104 GTGAGTGCAGCAGGAGATGAGATGAGATGATCCGGGAGAGAGAGCTGCCCTCTGC 2163
D 2518 GTGAGTGCAGGAGATGAGATGAGATGATGAGATGAGAGAGAGAGAGAGAGAGAGAG 2577
OY 2164 TTTGATCTAGCTCATGCACTTCTGACTGTCTTGTGGAAGTGTCTGTTGCTGTGCCC 2223
D 2578 TTTGATCTAGCTCATGCACTTCTGACTGTCTTGTGGAAGTGTCTGTTGCTGTGCCC 2637
OY 2224 CCCACAGAGTACGACGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2283
D 2638 CCGACAGAGTACGACGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2697
OY 2284 CTCACGCGCATTTGGGAGACCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2343
D 2698 CTCACGCGCATTTGGGAGACCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2757
OY 2344 TCAGTACAGCTGTCTTTTTCGTGGCATTTGGCAGCTCTGTCCAGATAGCTTGGCAG 2403
D 2758 TCCGTACCGCGGT 2817
OY 2404 AAAGTGTGCGGCTTCCAGAGTGTATGAGAGCGGCTCATTTGGGAGAGAGAGAGAGAG 2463
D 2818 AAAGTGTGCGGCTTCCAGAGTGTATGAGAGCGTATGATGATGATGATGATGATGATG 2877

OY 2464 AACGCCGTCAATGTCTTCTGGGACATGCGCTGGCTGTCCGTGGCCGACATCTAGG 2523
D 2878 AACCGGTGAACGCTTCTGGGACATGCGCTGGCTGTCCGTGGCCGACATCTAGG 2937
OY 2524 GCTTGTGAGGACAGAGTTCACAGTGTGGGCGGACACACTGGCTTCTGTCACCTC 2583
D 2938 GCGGCCAACGCGGAGAACGTTCAAAAGTGTCCCTGGCAGCTAGCTTTTCTGTACATCT 2997
OY 2584 TTACACATCTTTGATTTGTCTGATCAGGCTGTCTGTACGGAAGGCGGCGACCTG 2643
D 2998 TTACACATCTTTGATTTGTCTGATCAGGCTGTCTGTACGGAAGGCGGCGACCTG 3057
OY 2644 GGAAGGAGGCTTGGTGGCCCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2703
D 3058 GGAAGTGTGAGTGGTGGGCGGCGGACGCAAGCTCTCAATCTGCTTGTGTCTC 3117
OY 2704 CTGTGGCTCTCTACATCTTCTTGGCCACACTAGAGGCTTATGCTACATCAAGGGTTC 2763
D 3118 CTGTGGCTCTTGTACATTTCTTCTCTCTCTGAGGCGCTACAGCACAATAAGGCTTC 3177
OY 2764 TAA 2766
D 3178 TAA 3180

RESULT 7
ABV24305
ID ABV24305 standard; cDNA: 5438 BP.
XX
AC ABV24305;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 24296.
XX
KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
PN Homo sapiens.
XX
WO200160860-A2.
XX
23-AUG-2001.
XX
20-FEB-2001; 2001MO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1: Page 4554-4555; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

Db	493	CCTGAGGAGACCAAGTTCATGAGAGCCATACCCCTCACTGACGACGAGGGATGAGATGAGC	552
Qy	2132	ATGAATCCGGGAGAGAGAGGCTGCCCTCTGCTTTGACTACGTATGCTACTTCTCTGACTG	2191
Db	553	ATGAATCCGGGAGAGAGGCTGCCCTCTGCTTTGACTACGTATGCTACTTCTCTGACTG	612
Qy	2192	TCTTTCGGAAGTGCTGTTTGCTGTGTGTGCCCCCAGAGTACTGCCACGGCTGGGCT	2251
Db	613	TCTTTCGGAAGTGCTGTTTGCTGTGTGTGCCCCCAGAGTACTGCCACGGCTGGGCT	672
Qy	2252	GCTTGCGCCTTCATCCATCATTTGGCATGTGCMACCGCATCATTTGGGAGCCTGGGCT	2311
Db	673	GCTTGCGCCTTCATCCATCATTTGGCATGTGCMACCGCATCATTTGGGAGCCTGGGCT	732
Qy	2312	CGCACTTCGGCTGACACATTGTGCTCAAGATTCACTACAGCTGTGTTTCTGTGGCAT	2371
Db	733	CGCACTTCGGCTGACACATTGTGCTCAAGATTCACTACAGCTGTGTTTCTGTGGCAT	792
Qy	2372	TTGGCACCTCTGTCCAGATACGTTTGGCAGAAAGCTGTGCCCTCCAGAGTATATATG	2431
Db	793	TTGGCACCTCTGTCCAGATACGTTTGGCAGAAAGCTGTGCCCTCCAGAGTATATATG	852
Qy	2432	CAGAGCCCTCCATTTGGCAACGTACAGGGGAGCAAGCCGTCATGTCTTCTGTGGCATCG	2491
Db	853	CAGAGCCCTCCATTTGGCAACGTACAGGGGAGCAAGCCGTCATGTCTTCTGTGGCATCG	912
Qy	2492	GCTTGCCCTCTGTGACCGGAGGCGCCATGTACTGAGGCTGTGCAAGGGACAGAGTCCAGCTGT	2551
Db	913	GCTTGCCCTCTGTGACCGGAGGCGCCATGTACTGAGGCTGTGCAAGGGACAGAGTCCAGCTGT	972
Qy	2552	CGGCGGGACACATGCGCTTCTCCGTACACCCCTTTCACCATCTTTGACTTGTCTGCATCA	2611
Db	973	CGGCGGGACACATGCGCTTCTCCGTACACCCCTTTCACCATCTTTGACTTGTCTGCATCA	1032
Qy	2612	GCGTGTCTTTTACCCAGAGGCGGCGCACCTGGAGGGAGCTGTGTGGCCCCCGTGGCT	2671
Db	1033	GCGTGTCTTTTACCCAGAGGCGGCGCACCTGGAGGGAGCTGTGTGGCCCCCGTGGCT	1092
Qy	2672	GCAAGCTCCACCAACATGGCTCTTGTGTGAGCGCTGTGTCCTACATCTCTTGGCA	2731
Db	1093	GCAAGCTCCACCAACATGGCTCTTGTGTGAGCGCTGTGTCCTACATCTCTTGGCA	1152
Qy	2732	CACTAGAGCCCTATTGCTACATCAAGGGGTTCTTA	2766
Db	1153	CACTAGAGCCCTATTGCTACATCAAGGGGTTCTTA	1187
RESULT 9			
ABA64480			
ID	ABA64480	standard; DNA; 1836 BP.	
XX	AC	ABA64480;	
XX	DT	01-FEB-2002 (first entry)	
DE	XX	Human foetal liver single exon nucleic acid probe #12765.	
XX	XX	Human, foetal liver, gene expression; single exon nucleic acid probe; ss	
XX	OS	Homo sapiens.	
XX	PN	MO200157277-A2.	
XX	PD	09-AUG-2001.	
PF	XX	30-JAN-2001; 2001WO-US00669.	
PR	XX	04-FEB-2000; 2000US-0180312.	
PR	XX	26-MAY-2000; 2000US-0207456.	
PR	XX	30-JUN-2000; 2000US-0608408.	
PR	XX	03-AUG-2000; 2000US-0632366.	
PR	XX	21-SEP-2000; 2000US-0234687.	
PR	XX	27-SEP-2000; 2000US-0236359.	

PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-483447/52.
DR
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
PS
XX
XX Claim 4; SEQ ID NO 12785; 639pp + sequence listing; English.
CC
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;
SQ

[illegible]

```
OY 769 TTCTCAAAATACATGCACAAAAGTACCGACAGACAAACCGAGGAATTTATCATAGAG 828
  || || || || || || || || || || || || || || || || || || || || || ||
Db 793 TTTTACAAAGATATGCTACAGAGAGTATCGAGCTGGCAAGCAGAGGGGATGATTATGAA 852
OY 829 ACAGAGGGTGCACCC-----TAAAGGCAATTGAGATGGGAAAATGATGAAT 879
  || || || || || || || || || || || || || || || || || || || || || ||
Db 853 CATGMAAGGACACAGGCACTCTTCTMAAGCATGMAATTGMAATGAGCGGAAAGTGCTCAAT 912
OY 880 TCCCAATTTTGTAGTGGGAACCTGTGCTCCCTGGGAAGGGAAG----- 921
  || || || || || || || || || || || || || || || || || || || || || ||
Db 913 TCTCATTTTGAATAATTTCTTAGATGTGCTCTGTGTTCTGGAGGTGAGTGAAGGACCA 972
OY 922 GAAGTGTAGTCCCGCAGAGAGATGATCCGATTTCTCAAGATCTGAACAAAAAC 981
  || || || || || || || || || || || || || || || || || || || || || ||
Db 973 GATGATGAAGAGCTAGCGGCAAAATGGCTAGATCTGGAAGGAATTAAGCAGAACAT 1032
OY 982 CCAGAGAAGCACTTAGTCAAGCTGTGTGAGATGGCCAAATTAATGCTCTTTCCACCAA 1041
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1033 CCAGATTAAGAAATAGACATTAATAGAAATAGCTAACTCAACCAAGTCTAAGTCACAG 1092
OY 1042 CAGAGAAGCCGCGCTCTACCGATATCCAGCCACCTGTGATGATCTGGTGGAGCAAT 1101
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1093 CAAAAAAGTAGAGCATTTTATCCGATTCAGACTACTGCTCATGACTGGAGCTGGCAAC 1152
OY 1102 ATCCTGAAGAAACATGCGAGAGAAACAAGAGGCTCTCAGCATGAGCAGAGTGCAC 1161
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1153 ATTTTAAAGAGGATGCGAGTGCACCAAGCAAGGAAGGCTGACAGCATGCAAGAGTCAAC 1212
OY 1162 ACCGATAGGCTG---AGGACTTATTTCCAGAGTCTTCTTTGACCATGTTCTTACCAG 1218
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1213 ACTGAATGACTGAATAATGACCCCTGTAGTAAATCTTCTTGAACAAAGGACATACAG 1272
OY 1219 TGCTTGAGAACTGTGGGCTGTACTCTGACATGATGCTGAGAAAGGGGAGACATCA 1278
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1273 TGTCTGGAAGAACTGTGTACTGTGCGCTTACCACTTATCCGACAGAGTGGTGAATTAAT 1332
OY 1279 AAGACATGATGTGACTACAAAACAGAGAGATGTTCTCCCAATGACAGGGGCTGACTAT 1338
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1333 AACACTGTGTTGTGACTTCAGAACAGAGATGGACACCAATAATGCTGGGTCTGATTAAT 1392
OY 1339 GAGTTCACAGAGGCGAGGTGTTCTGAACCCAGAGAGACCCAGAAAGAGTCTCCGTG 1398
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1393 GAATTTACTAGAGAACTGTGGTGTAAAGCTGTGATACCCAGAAAGAAATCAGAGTG 1452
OY 1399 GGCATTAATGATGACGACTTTTGGAGAGATGAACACTTCTTGAAGTTGAGCAAT 1458
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1453 GGTATCATATGATGATGATCTTTGAGAGAGATGAATAATTTCTTGTGCAATCTCAGCAAT 1512
OY 1459 GTCCGATAGAGGAGAGCAGCAGAGAGAGGGGATGCCCTCCAGCAATATTTCAACAGTCTT 1518
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1513 GTCAAAAGTATCTCTGAAAGCTTCAGAAAGATGGCATTAAGTGAAGC-----CAATCAT 1563
OY 1519 CCTTGGCTGGGCTGTCTCAGAGCTCCCTTGTGTGCGCCACAGTATTAATCTTGGATGAT 1578
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1564 GTTCTTACACTTCTGCTCCGATCTCCCTCCACTGCACTGCACTGCACTGCACTGCACTG 1623
OY 1579 GACCATCAGAGCACTCTCACTTTTGAATGTGATACTATTCATGATGATGAGATGATGAT 1638
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1624 GACACAGCAGAGCACTTTTACTTTTGAAGAACTGTGACTCATGTGATGATGAGCATTGGC 1683
OY 1639 GTTATGAGAGTCAAGTCTTGCAGACATCAGGTGCCCGGGGTACAGTCAATGTCCTCTT 1698
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1684 ATCATGAGAGTGAAGATTTGAGAACATCTGGAGCTCGAAGGAATTTATCTTCCATAT 1743
OY 1699 AGCAGACTAGAGGAGCAGCAAGGCTGGCGGTGAGAGACTTTGAAGACACATATGGGAG 1758
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1744 AAAACCACTCAAGGAGACTGCGCAGAGGTGAGGAGGAGGATTTTGAAGACACTTGTGAGAG 1803
OY 1759 TTGGAATTTCAAGATGATGAACGTGAAA 1788
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1804 CTGGAATTTCCAGAAATGATGAATTTGTAA 1833
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RESULT 10
ABA31619
ID ABA31619 standard; DNA; 1836 BP.
XX
AC ABA31619;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #10085 for gene expression analysis in human heart cell sample.
XX
KW Human: gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000US-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
PS Claim 4; SEQ ID NO 10085; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;
XX
Query Match 28.5%; Score 787.2; DB 22; Length 1836;
Best Local Similarity 68.3%; Pred.No.3.9e-216;
Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;
OY 109 GAGTGCCACAGCAGAGGAGGAGACAAATGAGTCCCTGTTCAGAGGTCATCGACTCAAGAG 168
  || || || || || || || || || || || || || || || || || || || || || ||
Db 133 GAATGGAAGAGAGAGAAATGAATGAGTGGATGATCTGATCATATTAATTAAGAA 192
OY 169 GTGTCTATCTCTGCCAATCTGTGTAACCGGAGAACCTTCCCTTGGGCAAGATTCAGAG 228
  || || || || || || || || || || || || || || || || || || || || || ||
Db 193 GGGGTGATTTTGGCCATTTGGGAACCCCAAGACCTTCTTTTGGGGCAAAATTTGCTAGA 252
OY 229 GTCATGTCTAATTTTGGGCGCCGATATATATCTTCTGGGTGCCATCATTTGCTGAC 288
  || || || || || || || || || || || || || || || || || || || || || ||
Db 253 GCTACTGTGATTTTGGGCGCATGCTCTACATCTTTCTTGAATCTCTATACATAGCTGAT 312
OY 289 CGCTTCATGCACTATTAATGAATCATCACCTCTCAAGAGAGGAGTGAACATTAAGAAA 348
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Db 313 CGGTTCATGTCCTCTATAGAAATCATCTCAAGAAAAAATAACCTTAAGAAA 372
Qy 349 CCCAATGAGAAACGACACAAACCACTATTGGGCTCGAATGAACCTGTCCAACTG 408
Db 373 CCCAATGAGAGACCAACCAAGCACTGTGAAGATCTGGAATGAAGAGTTCTTAACCTG 432
Qy 409 ACCCTTAAGGGCCCTGGTCCCTGCTGATGACTGCTCTTTAATGAGTGTGT 468
Db 433 ACCTTGATGGCCCTGGGATCTTCTGCTCTGATTCCTCTTCACTAATGAAGTGTGT 492
Qy 469 GGTCAATGGGTTCACTGCTGCTGATCTGGACCTTCACTAATGTAGGAGTCCACCTTC 528
Db 493 GGCAATACCTTCACTGCGAGGAGACCTGGGTCTTACACCAATGCTGGAAGTCTGCATTC 552
Qy 529 AACATGTTCAATCATCTGATGCACTGTGTCTACGTGATCCACGAGAGACATGCGAAG 588
Db 553 AATATGTTCAATCATCTGATGCACTGTGTGTATGTGTGCTGACGAGAGACAAGAGAG 612
Qy 589 ATCAAGCATCTACGAGTCTCTTCATCAACGCTGCTGGAGTATCTTGCCATACAGTGG 648
Db 613 ATTAAGCATTTGCGTCTCTCTTGTGACAGCAGCTGGAGCATTTTGCTTACACTGG 672
Qy 649 CTCTATATGATTTGCGAGTCTTCTCCCTGGTGTGTCTCAGAGTTGGGAAGCCCTCTC 708
Db 673 CTTTACATTAATTTTGTCTGTCTATCTCTGCTGTGTGTGAGAGTCTGGGAAGTTTGTCT 732
Qy 709 ACTCTCTTCTTCTTCCAGTGTGTCTCTCTGCTGCTGGGTGGCAGATTAACGACTGCTC 768
Db 733 ACTTCTCTTCTTCTTCCATCTGCTGTGTGTCTGCTGCTGGGTAGAGAGACTTCTG 792
Qy 769 TTCTCAATATCATGCAAAAAAGTACGCAACAGCAAAACCGAGGATTTATCATAG 828
Db 793 TTTTCAAGTATGTCTACAGAGTATGAGCTGGCAAGCAAGGAGATTTATGAA 852
Qy 829 ACAGAGGCTGACCAACC-----TAAGGCAATTGAGATGAGGAAATGATGAAT 879
Db 853 CATGAAGAGACAGGCACTCTTAAGACTGAATTTGAATGAGAGGGAATGTGATCAT 912
Qy 880 TCCCATTTTCTAGATGGAACTGTGCTGCTGGAAGGAG----- 921
Db 913 TCTCATGTGAAAAATTTCTTGAATGCTGTGCTGTCTGAGAGTGGATGAGAGACCA 972
Qy 922 GAAGGATGAGTCCCGAGAGAGATCCGGAATTCAGAGATCTGAAGCAAAAAAC 981
Db 973 GATGATGAAGAGCTAGAGCGAAGAAATGCTAGATTTGAAAGAACTTAAGCAAGCAT 1032
Qy 982 CCAGAGAGAGACTTATGATCAGCTGTGAGATGGCCAAATTACTATGCTTTCCACCA 1041
Db 1033 CCAGATTAAGAAATAGACCAATTAATAGATTAAGTACTACCAAGTCTTAAGTACAG 1092
Qy 1042 CAGAAAGCCCGCTTACCCTTACCGATCAAGCCACTGCTATGATGATGCTGAGCAAT 1101
Db 1093 CAAAAAATAGAGCAATTTATGCAATCAAGCTACTCGCTCATGACTGAGAGCTGCAAC 1152
Qy 1102 ATCTGAGAAACATGCGAGCAAGCAAGAGGCTCCAGATGAGCGAGGTGCGAC 1161
Db 1153 ATTTAAAGAGCATGACGCTGACCAAGCAAGAGGCTGATGATGACGAGGTCAAC 1212
Qy 1162 ACCGATGAGCCTG---AGGACTTTATTTCCAGAGTCTTCTTTGACCCATGCTTACAC 1218
Db 1213 ACTGAAGTACTGAAGAAATGACCCCTGTAGTAAATCTTCTTTGAACAAAGGACATAC 1272
Qy 1219 TGCCTGAGAACTGTGGGCTGTACTCTGACAGTGTGAGAGAAAGGGGAGACATGTCA 1278
Db 1273 TGTCTGAGAACTGTGTACTGTGGCCCTTACCATTAATCCGAGAGTGTGATTTGACT 1332
Qy 1279 AAGACATGATGATGAGTACTACAAACAGAGAGATGTTCTTGCCAAATGCGAGGCTACTAT 1338
Db 1333 AACACTGTGTTGTGACTTCAAGAACAGAGATGACACGCAAAATGCTGTGATATAT 1392
Qy 1339 GAGTTACAGAGAGGACGCTGTGTTCTGAAGCCAGAGAGACCAAGAGATTCCTCCGTG 1398
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Db 1393 GAATTTACTGAAGAACTGTGGTGTAAAGCTGTGATACCCAGAGAAATACAGAGTG 1452
Qy 1399 GGCATTAATTTGATGAGACATTTTGTAGAGATATGAACATCTTGTATAGTTGACAT 1458
Db 1453 GGTATCATAGATGATGATATCTTTGAGAGATGAAGAAATTTCTGTGATCTACAGCAT 1512
Qy 1459 GTCCCATGAGAGAGAGACGAGAGAGGAGATGCCCTCCAGAAATATTAACAGTCTT 1518
Db 1513 GTCAAGATATCTTCTGAACTTCAGAGATGCAATGCTACTGTAAGC-----CAATCAT 1563
Qy 1519 CCCTTGCTCGGCGTGTCTACCTCCCTTGTGTGGCCACAGTTACCATCTTGATAT 1578
Db 1564 GTTTTACACTGCTGCTGCTGATCTCCCTCAGTCCAGTACATGTAATTTTGTATGAT 1623
Qy 1579 GACCATGCAAGGATCTTCACTTTTGAATGTGATTAATCATGTCAGTACAGTATGCT 1638
Db 1624 GACCAAGGAGGATTTTCACTTTTGAAGACCTGTGACATGATGTGAGAGCATGTC 1683
Qy 1639 GTTATGAGAGTCAGATGTCGAGCATCAGGTCGCCGGGTACAGTCACTGCTCCCTTT 1698
Db 1684 ATCATGAGAGTGAAGATATTGAGAACATCTGAGACTCGAGAAATGTTATCTTCCATAT 1743
Qy 1699 AGGACAGTGAAGAGGACAGCAAGGATGGCGGTGAGAGCTTTGAAGACATATGGGAG 1758
Db 1744 AAACCATGAGAGGAGCTGCGAGAGGTGAGAGGAGATTTTGAAGACATTTGTGAGAG 1803
Qy 1759 TTGGAATTCAGAAATGATCAAACTGTGAAA 1788
Db 1804 CTCGAATTCAGAAATGATGAAATTTGTAA 1833

RESULT 11
AAK12937
ID AAK12937 standard; DNA: 1836 BP.
XX
XX AAK12937;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX
DE Human brain expressed single exon probe SEQ ID NO: 12928.
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
OS Homo sapiens.
XX
XX WO200157275-A2.
PN
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
PR
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483446/52.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
XX Example 4; SEQ ID NO: 12928; 650pp + Sequence Listing; English.
PS
XX The present invention provides a number of single exon nucleic acid
XX
XX
```

CC probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.

XX Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;

Query Match 28.5%; Score 787.2; DB 22; Length 1836;
Best Local Similarity 68.3%; Pred. No. 3.9e-216;
Matches 1188; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

QY 109 GAGGTGCAAGCAGAGGAGGAGCAATGAGTCTCTTCAAGGTCATCGACGCAAGAG 168
DB 133 GAATGGAAGAGAGAAATGAAACGTGGAATGATCTGATCATATTTCTGTAAGAAA 192
QY 169 GGTGTCTCTCTCCCAATCTGTGACCGGAGAACCTTCCCTGGGACAAAGATTGCCAG 228
DB 193 GGGGTGATTTTGGCCATTTGGGAAACCCCAAGACCTTCTTTGGGGCAAAATTTGCTAGA 252
QY 229 GTGATGTCATTTTGGGCGCTGATATATGATGTCCTTGGGGTCCATCATTTGCTGAC 288
DB 253 GCTACTGTGATTTTGGGCGCTGATATATGATGTCCTTGGAGTCTTATCATAGCTGAT 312
QY 289 CGCTTCATGCGCATATATGAGTCAATCCTCTCAAGAGAGGAGTGAACATTAAGAAA 348
DB 313 CGGTTCATGTCCTCTATAGAAAGTCAATCATCAAGAAAAGAAATTAACATTAAGAAA 372
QY 349 CCCAATGAGAAACACAGACACCAATATTCGGGTCTGGAATGAATGTCCTCAACCTG 408
DB 373 CCCAATGAGAAACACCAAGCAACATGAGATCTGGAATGAATGAATGTCCTCAACCTG 432
QY 409 ACCCTTATGCGCGCTGCTCTGCTGCTGATATCTCTCTTAAATTAATGAGTGTG 468
DB 433 ACCCTTATGCGCGCTGCTCTGCTGCTGATATCTCTCTTAAATTAATGAGTGTG 492
QY 469 GGTTCATGCTTCATGCTGCTGATCTGAGACCTTCAACATTTGAGGAGTGAACCTT 528
DB 493 GGGCATATCTTCATCTGAGAGACCTGCGTCAAGCAATCGTGGGAAGTCTGATTC 552
QY 529 AACATGTCATCATATGAGTGTGCTGATCTGATCCAGAGAGAGTCTGCAAG 588
DB 553 AAATATGTCATCATATGAGTGTGATGCTGATGCTGAGAGAGAGTCTGCAAG 612
QY 589 ATCAAGATCTAGAGTCTTCTCATACCGCTTGAAGTATCTTGGCTATATCTG 648
DB 613 ATTAAGATCTTGGCTGCTCTTCTGATGAGAGAGTCTGAGATCTTGGCTATATCTG 672
QY 649 CTCTATATGATCTGAGTCTTCTCTGCTGCTGCTGCTGAGTCTTGGAGAGGCTCTC 708
DB 673 CTCTATATGATCTTCTGCTGCTGCTGCTGCTGCTGCTGAGTCTTGGAGAGGCTCTC 732
QY 709 ACT 768
DB 733 ACT 792
QY 769 TTTTCAAAATATATGCAAGAAAGTACCGACAGACAAACGAGAAATTAATATGAG 828
DB 793 TTTTCAAAATATGCTTCAAGAAAGTATGAGAGTATGAGAGAGGAGGATTAATGAA 852
QY 829 ACAAGAGGTGACCAACC-----TAAGGCAATGAGATGGAATGAATATGATGAAT 879
DB 853 CATGAAGAGAGAGGAGGATCTCTTCAAGATGGAATTAATGAATGAGAGGAGAAATGCTCAAT 912
QY 880 TCCCATTTTCTAGATGGAACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921
DB 913 TCTCATTTTCAAAATTTCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
QY 922 GAAGTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981
DB 973 GATGATGAAGAGCTAGGAGAGAAATGCTGAGATTTCTGAAGCACTTAAGCAGAACCAT 1032

QY 982 CCAGAGAGAGCTTATGATCACTGTGTGAGATGGCCATTAATTAATGCTCTTTCCACCAA 1041
DB 1033 CCAGATTAAGAGAAATATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1092
QY 1042 CAGAGAGCGCGCT 1101
DB 1093 CAAAGAAAGTATGAGCAATTTATGATTTCAAGCTCTGCTCATGACTGAGGCTGGGCA 1152
QY 1102 ATCCTGAGAAACATGAG 1161
DB 1153 ATTTTAAAG 1212
QY 1162 ACCGATGAGCTG---AGACCTTATTTTCAAGGCTCTCTCTCTCTCTCTCTCTCTCT 1218
DB 1213 ACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1272
QY 1219 TGCTGAGAGAGTGTGGGCTGATCTCTGACAGTGTGTGAAGAAAGGGGAGAGATGCA 1278
DB 1273 TGCTGAGAGAGTGTGGGCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1332
QY 1279 AAGACATATGATGAGTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1338
DB 1333 AAGACATATGATGAGTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1392
QY 1339 GAGTTCAG 1398
DB 1393 GAATTTCTGAG 1452
QY 1399 GGCATATATGATGAG 1458
DB 1453 GGTATCATATGATGAG 1512
QY 1459 GTCCGATTAAG 1518
DB 1513 GTCAAGATATCTTCTGAG 1563
QY 1519 CCTTGGCTGAG 1578
DB 1564 GTTCTCATATGAG 1623
QY 1579 GACCATGAG 1638
DB 1624 GACCATGAG 1683
QY 1639 GTTATGAG 1698
DB 1684 ATCATGAG 1743
QY 1699 AGCAG 1758
DB 1744 AAACCATGAG 1803
QY 1759 TTGGAATTTCAAGATGATGAATCTGAAA 1788
DB 1804 CTGGAATTTCAAGATGATGAATCTGAAA 1833

RESULT 12
AA119464
ID AA119464 standard; DNA: 1836 BP.
XX
AC AA119464:
XX
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #9397 for gene expression analysis in human cervical cell sample.
XX
KM Probe: human; microarray; gene expression; cervical epithelial cell;
XX
OS cervical cancer; ss.
XX
PN Homo sapiens.
WO200157278-A2.

xx 09-AUG-2001.
pd 30-JAN-2001; 2001WO-US00670.
xx
xx 04-FEB-2000; 2000US-0180312.
xx 26-MAY-2000; 2000US-0207456.
xx 30-JUN-2000; 2000US-0608408.
xx 03-AUG-2000; 2000US-0632366.
xx 21-SEP-2000; 2000US-0234687.
xx 27-SEP-2000; 2000US-0236359.
xx 04-OCT-2000; 2000GB-0024263.
xx
xx (MOLE-) MOLECULAR DYNAMICS INC.
xx Penn SG, Hanzel DK, Chen W, Rank DR;
xx WPI; 2001-488901/53.
xx
xx Human genome-derived single exon nucleic acid probes useful for
xx analyzing gene expression in human cervical epithelial cells -
xx
xx Claim 25; SEQ ID No 9397; 487bp; English.
xx
xx The present invention relates to human single exon nucleic acid probes
xx (SENPs). The present sequence is one such probe. The SENPs are derived
xx from human HeLa cells. The SENPs can be used to produce a single exon
xx microarray, which can be used for measuring human gene expression in a
xx sample derived from human cervical epithelial cells. By measuring gene
xx expression, the probes are therefore useful in grading and/or staging
xx of diseases of the cervix, notably cervical cancer.
xx Note: The sequence data for this patent did not form part of the printed
xx specification, but was obtained in electronic format directly from WIPO
xx at ftp.wipo.int/pub/published_pcf_sequences.
xx
xx Sequence 1836 BP: 512 A; 336 C; 464 G; 524 T; 0 other;
xx
xx Query Match 28.5%; Score 787.2; DB 22; Length 1836;
xx Best Local Similarity 68.3%; Pred. No. 3,9e-216;
xx Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;
xx
xx 109 GAGCTGCCAAGCAGGAGGAGCAATGATGCTCTTCAGGCTATCGAGCTGCAAGAG 168
xx 133 GAAATGGAGAGGAGGAAATGAATGCTGATGATGATGATGATGATGATGATGATG 192
xx 169 GGTGTCATCTCCCAATCTGTACCCGGAACCTTCCCTTGGGAGCAAGATTGCCAG 228
xx 193 GGGGTGATTTTCCCATTTTGGGAGACCCCAAGACCTTTCTTTGGGACAAAATTGCT 252
xx 229 GTCATTTGCTATTTTGTGCGCTGATATGATGATGATGATGATGATGATGATGAT 288
xx 253 GCTACGTGTATTTTGTGCGCTGATGATGATGATGATGATGATGATGATGATGAT 312
xx 289 GCGTCATGAGCATATTTAATGATCATTACCTCAAGAGAGAGAGTGAATTAAGAA 348
xx 313 CGGTTCATGCTCTCTATAGATCATTCAATCTCAAGAAAGAAATTAACATTAAGAA 372
xx 349 CCCAATGGAGAAACGACCAACACTATTCGGGTCTGGAATGAACCTGTCTCAAC 408
xx 373 CCCAATGGAGAAACGACCAACACTATTCGGGTCTGGAATGAACCTGTCTCAAC 432
xx 409 ACCCTTATGAGCCCTGGGTCTCTGCTCTGATGATGATGATGATGATGATGATGAT 468
xx 433 ACCCTTATGAGCCCTGGGTCTCTGCTCTGATGATGATGATGATGATGATGATGAT 492
xx 469 GGTGATGGGTGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 528
xx 493 GGCCTAATCTTCACTGAGAGAGACCTCGGTCTCTAGACCATGCTGGGAAGTCTGAT 552
xx 529 AACATGTTTCATCATTTGGCATCTGTGTCTAGCTGATCCAGACGAGAGATCGCAAG 588
xx 553 AATATGTTTCATCATTTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 612

QY 589 ATCAGCATCTACGAGTCTCTTTCATCACCGCTGAGATGATCTTGGCCATCTCG 648
DB 613 ATTAAGCATTTCCGTGTCTCTTCTTGTGACAGCAGCTGGAGATCTTTCCTACAC 672
QY 649 CTCTATATGATTTGGGAGCTTCTCCCTGCTGTGTCAGAGTTTGGAGAGCCCTCTC 708
DB 673 CTTTACATATTTTGTGTGATATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 732
QY 709 ACTCTCTCTTCTTCCAGTGTGTCTCTCTGCGCTGGGTGGCAGATTAAGCATCTGC 768
DB 733 ACTTCTCTCTTCTTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 792
QY 769 TTCTCAATATACATGCAAAAAGTACCGCACAGACAAACAGCAGGAAATTAATAG 828
DB 793 TTTTACAGTATGCTTACAGAGATATCGAGCTGGCAGCAGAGGGGATGTTTGA 852
QY 829 ACAGAGGTGACACCC-----TAAGCATTTGAGATGATGATGATGATGATGAT 879
DB 853 CATGAAGGAGACAGGCATCTTCTAAGACTGAATTTGAATGAGAGGGGAAATGTCAT 912
QY 880 TCCCATTTTCTGATGAGGAGCTGTGCTGCTGGAAGGAG----- 921
DB 913 TCTCATGTTGAAAATTTCTTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 972
QY 922 GAAGTGATGATCCCGCAGAGAGATGATCCGATTTCTCAAGATCTGAAGCAAAACAC 981
DB 973 GATGATGAAGAGCTTAGGCGAGAAATGCTAGGATTTCTAAGCAATTAAGCAAGAA 1032
QY 982 CCAAGAAAGACTTAGATCAGCTGTGTGAGATGAGCCAAATTAATGCTTTTCCACCA 1041
DB 1033 CCAGATTAAGAAATGAGCAATTAATAGAAATAGCTAATCAACAGTCTAAGTACG 1092
QY 1042 CAGAAGAGCCGCGCTTACCTGATCCAGGATCTGATGATGATGATGATGATGATG 1101
DB 1093 CAAAAAGTAGAGCAATTTATGCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1152
QY 1102 ATCTGAAAGAACATGACAGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1161
DB 1153 ATTTTAAAGAGCATGACAGCTGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1212
QY 1162 ACCGATGAGCTG---AGGACTTATTTTCAAGGCTCTTGTGACCATGTTCTTAAC 1218
DB 1213 ACTGAAGTACGAAATGAGCAATTAATAGATTTAGATCTTCTTGAACAAAGGACAT 1272
QY 1219 TGCCTGAGAACTGTGGGCTGTACTCTGACAGTGTGATGAGAAAGGGGAGACAT 1278
DB 1273 TGTCTGAGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1332
QY 1279 AAGACCATGATGTGACATCAAAAACAGAGATGATGATGATGATGATGATGATGAT 1338
DB 1333 AACACTGT 1392
QY 1339 GAGTTTCAGAGAGGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1398
DB 1393 GATTTTACGAAAGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1452
QY 1399 GGCATATATGATGACACATTTTGTGAGAGATGAACATCTTGTTAAGGTGAGCAT 1458
DB 1453 GGTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512
QY 1459 GTCCGATAG 1518
DB 1513 GTCAAAATGATCTTGTGAAGCTTCAAGAGTGCATGATGAGAGC-----CAAT 1563
QY 1519 CCTTGCCTCGGGCTGTCTACGCTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1578
DB 1564 GTTTTACAGCTGTGCTGCTGCGATCTCCCTCACTGACAGCTAATTTTGTGATG 1623
QY 1579 GACCATGACGAGATCTTCACTTTTGAATGATGATGATGATGATGATGATGATG 1638
DB 1624 GACCAAGCAGGAGATTTTACTTTTGTGAGAACTGTGACTCATGTGATGAGAGAT 1683
QY 1639 GTTATGAGAGTCAAGGTTGTGGGACATCAAGGTCGCCGGGGGTACATGATCGTCC 1698

Db 1684 ATCATGAGGTGAAGATGATTGAGAACATCTGAGCTCGAGGAATGTTATCGTTCCATAT 1743
Oy 1699 AGGACATAGAGGAGAGGACAGGCGGTGAGACATTTGAAACACATATGGGAG 1758
Db 1744 AAAACCTTCAGAGGACTGCGACAGGTGAGGAGGATTTTGAGACACTGTGGAGAG 1803
Oy 1759 TTGGATTTCAAGATGATGAAGACTGTGAAA 1788
Db 1804 CTGCAATTCAGAAATGATGAATGTGTAA 1833

RESULT 13
AA144657
ID AA144657 standard; DNA; 1836 BP.
XX AA144657;
AC
XX
XX
XX 17-OCT-2001 (first entry)
DE Probe #13343 used to measure gene expression in human placenta sample.
XX Probe: microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; 99.
XX Homo sapiens.
XX MO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001MO-US00663.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID NO 13343; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders.
XX
XX Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;

Query Match 28.5%; Score 787.2; DB 22; Length 1836;
Best Local Similarity 68.3%; Pred. No. 3,9e-216;
Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

Oy 109 GAGTGGCAAGCAGGCGAGAACATGAGTCCGTTCAGAGGTCATGGACATGCAAGAG 168
Db 133 GAATGGAAGAGAGAAATGAAGCTGTGAATGTAAGTATTTACTGTAAAGAA 192
Oy 169 GGTGTCACTCCGCAATCTGTACCCGAGAACCTTCCTTGGGAGACAGATTGACAG 228
Db 193 GGGGTGATTTTGGCCATTTTGGAAACCCCAAGACCTTCTTTGGGAGCAAAATTTGCTAGA 252
Oy 229 GTCAATGTCTAATTTTGTGGCCCTGATATATACATTTCTTGGGGGTGTCATCATTTGCTGAC 288

Db 253 GCTCATGTGATTTTGTGGCCATGCTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT 312
Oy 289 CGCTCATGGCATCTATTTGAAGTATCATCCTCTCAAGAGGAGGAGACATTAAGAAA 348
Db 313 CGGTTCATGTCTCTATAGAAGTATCATCTCAAGAAAAAATAACCATTAAGAAA 372
Oy 349 CCCAATGAGAAACACAGCAACACACTATTGCGGTCTGGAATGAACCTCTCCAACTG 408
Db 373 CCCAATGAGAGACACACCAAGACACACTGTGAGATCTGGAATGAACAGTTTCAACCTG 432
Oy 409 ACCCTTATGGCCCTGGGCTCTCTGCTCTGAGATCTCTCTCTTTTAATTTGAGGTGT 468
Db 433 ACCCTTATGGCCCTGGGATCTCTGCTCTGAGATCTCTCTCTTCAAGTAATTTGAGTGT 492
Oy 469 GGTCAATGGGTCATGCTGTGATCTGTGAGACCTTCTACATTTGAGGATGAGACCTTC 528
Db 493 GGCATTAACCTTCACTGAGAGAGACCTGTCTGATGACACCATCTGGAAGCTGTGACTTC 552
Oy 529 AACATGTTCAATCATTTGAGCATCTGTCTACGTCGATGATCCAGAGAGAGACTGCAAG 588
Db 553 AATATGTTCAATCATTTGAGCATCTGTCTTATGTTGTCGTCGAGAGAGACAGAA 612
Oy 589 ATCAAGCATCTAGAGTCTTCTTCATCAGCGCTGCTTGGAGTATCTTTCCTACATCTG 648
Db 613 ATTAAGCATTTGGCTGTCTCTTGTGACAGACACCTGAGACATCTTGGCTACACTG 672
Oy 649 CTCTATGATGATTCGGGAGTCTCTCCCGGTGTGTCGAGTTGGGAAGGCTCTC 708
Db 673 CTTTACATTAATTTTGTGTGTCATATCTCTGTGTGTGTGAGAGGTCTGGAAAGTTGCTT 732
Oy 709 ACT 768
Db 733 ACT 792
Oy 769 TTCTACAATACATGACAAAGAGTACCGACAGACAAACGAGATTTATCATATGAG 828
Db 793 TTTTACAAGTATGTCACAAAGAGTATCGAGCTGCGACAGAGGCGAGATTTATTTAA 852
Oy 829 ACAGAGGTGACCAACC-----TAAGGCACTTGAATGATGGAATGATGAT 879
Db 853 CATGAAGAGACAGGACCATTTCTAAGCATGAATGAATGAAGGAGAGGTGCTCAAT 912
Oy 880 TCCCATTTCTAGATGGGAAGCTGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 921
Db 913 TCTCATGTTGAAAATTTCTTATAGATGCTGTCTGTCTGTGAGGATGATGAGAGACCA 972
Oy 922 GAAGTGTATAGTCCCGACAGAGATGATCCGATTTCTCAAGATCTGAAGCAAAACAC 981
Db 973 GATGATGAAAGCTAGGCGAGAAATGCTGAGATTTCTGAAGCAACTTAAGCAGAAACAT 1032
Oy 982 CCAGAGAGAGACTTAGATCAGCTGTGAGATGAGCCAAATTAATGCTTTTCCACCAA 1041
Db 1033 CCAGATTAAGAAATAGAGCAATTAATGAAATAGCTAATCAACCAAGCTTAAGTACAG 1092
Oy 1042 CAGAAGAGCCGCGCTTCTACCTATCAAGCAACCTGTATGATGACTGTGACCAAT 1101
Db 1093 CAAAAAAGTAGAGCATTTTATCCATCAAGCTATGCTGCTCTCATGACTGAGGCTGCAAC 1152
Oy 1102 ATCTCTGAAGAAATGAGACAGAAACCAAGAGGCTCCAGCATGAGAGGCTGCAC 1161
Db 1153 AATTTTAAAGAGGATGAGCTGACCAAGAGAGGCTGTGACAGTACAGAGGTCAAC 1212
Oy 1162 ACCGATGAGGCTG---AGAGCTTATTTCCAGAGCTCTTTGACCATTTCTTTACAG 1218
Db 1213 ACTGAAGTACTGAAAATGACCTGTTAGTAAATCTTTTGAACAAGGACATATACAG 1272
Oy 1219 TGCTGTGAGAACTGTGGGCTGTACTCTGACAGTGTGAGAAAGGAGAGACATGCA 1278
Db 1273 TGCTGTGAGAACTGTGTACTGTGGCCCTTACATTTATCCGAGAGGTGTGATTTGACT 1332
Oy 1279 AAGACATGTATGTGACTCAAAAACAGAGATGTTCTCCAAATGAGGCGCTGACTAT 1338
Db 1338

Db 1333 AACACTGTTGTTGACTTCAGAACAGAGATGGCAGACGAATGCTGGTGTGATAT 1392
 Oy 1339 GAGTTCACAGAGGAGGACGGTGTCTGAAAGCCAGAGAGACCCAGAGATTCCTCCG 1398
 Db 1393 GAAATTAAGTGAAGGAGAGTGGTGTAAAGCTGGATACCCAGAGAAATTCAGAGTG 1452
 Oy 1399 GGCATTAATGATGACACATTTTGGAGAGATGAACACTTCTTTGTAAGTTGAGCAAT 1458
 Db 1453 GGTATCATAGATGATATATCTTTGAGAGAGATGAATAATTCCTTGTGATCTGAGCAAT 1512
 Oy 1459 GTCCGCATAG 1518
 Db 1513 GTCAAGATATCTTCTGAAGCTTCAGAAAGATGGCATACTGGAAGC-----CAATCAT 1563
 Oy 1519 CCCTTGCTCGGGCTGTCTTACCTCCCTTGTGTGGCCACAGTTACCATTTTGATGAT 1578
 Db 1564 GTTCTTACACTGTTGCTGCTCGGATCTCCCTCAGCTCCAGCTGAATCTTTTGTATGAT 1623
 Oy 1579 GACCATGAGGAGCATCTTCACTTTGATGATGATGATGATGATGATGATGATGATGAT 1638
 Db 1624 GACCAAGGAGGAGCATTTTACTTTTGAAGACCTGTGACATCATGTGATGAGAGCATTTGGC 1683
 Oy 1639 GTTATGAGAGTCAAGGTTCTGCGGACATCAGTGTCCCGGGGTACAGTCAATCTCCCTTT 1698
 Db 1684 ATCATGAGAGTGAAGATATTTAGAACATCTGGAGCTCGAGAAATGTTATCTTCATAT 1743
 Oy 1699 AGGACAGTAGAAGGAG 1758
 Db 1744 AAAACCATCAGAGGAG 1803
 Oy 1759 TTGGAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1788
 Db 1804 CTCGAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833

RESULT 14
 ABS12734
 ID ABS12734 standard; DNA; 1836 BP.

AC ABS12734;

DT 19-AUG-2002 (first entry)

DE Human genome-derived single exon probe ORF from lung SEQ ID No 12725.

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KM Chronic obstructive pulmonary disease; interstitial lung disease;
 KM familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KM tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KM Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KM pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenet syndrome;
 KM pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KM primary ciliary dyskinesia; pulmonary hypertension;
 KM hyaline membrane disease; open reading frame; ORF.

OS Homo sapiens.

PN WO200186003-A2.

PD 15-NOV-2001.

PE 30-JAN-2001; 2001WO-US00665.

PR 04-FEB-2000; 2000US-180312P.

PR 26-MAY-2000; 2000US-207456P.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-234687P.

PR 27-SEP-2000; 2000US-236359P.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 PS
 XX Claim 4: SEQ ID No 12725; 634bp; English.

The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the labeled nucleic acids bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagenet syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a single exon
 CC probe open reading frame of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;

Query Match 28.5%; Score 787.2; DB 24; Length 1836;

Best Local Similarity 68.3%; Pred. No. 3; 9e-216;

Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

Oy 109 GAGCTGCCAAGCAGCAGCAGCAAGCAATGAGTCTGTCAGGTCATCGAGCAAGAGAG 168
 Db 133 GAAATGAG 192
 Oy 169 GGTGTCATCTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 228
 Db 193 GGGGTGATTTTGGCCATTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
 Oy 229 GTTCATGTCATTTTGGCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 288
 Db 253 GCTAGTGTGATTTTGGCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 312
 Oy 289 CGCTTATGCGCATCTATTGAGATCATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 348
 Db 313 CGGTTCATGTCCTCTATAGAGATCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
 Oy 349 CCCAATGAG 408

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Db      373  CCCAATGAGAGACACCAACACGTGAGATCTGGAAATGAACAGTTTCAACCTG 432
Oy      409  ACCCTTAGGCCCCGGGTCCTGCTGCTGAGATACCTCTTTTAATGAGCTGT 468
Db      433  ACCCTTAGGCCCCGGGATCTTCTGCTGCTGAGATTTCTCTTTAGTAATGAAAGTGT 492
Oy      469  GGTGATGGGTTCAATGCTGTGATCTGGACCTTCTACATTTGTAAGGAGTGACCTTC 528
Db      493  GGCATTAACCTCACTGAGAGACCTGCTGCTAGCACATCGTGGGAAGTGTGATTC 552
Oy      529  AACATGTTCAATCATATGGCATCTGTGTCTACTGATCCAGACGGAGAGACTCGAAG 588
Db      553  AATATGTTCAATCATATTAATGACACTGTGTGTTATGTGTGCTGACGAGAACAGAG 612
Oy      589  ATCAAGATCTACGAGTCTTCTTCATCACGCTGCTTGAAGTATCTTGGCTACATCTG 648
Db      613  ATTAAGCATTTGGCTGTCTTCTTGTGACAGACGCTGAGACATCTTGGCTACACTGG 672
Oy      649  CTCTAATATGATTCGCAAGTCTTCTCCCTGCTGTGCTCAAGTTTGGGAAGCCCTCTC 708
Db      673  CTTAACATTAATTTGTTGCTGATATCTCTGCTGTGAGGTGCTGGAAAGTTGCTT 732
Oy      709  ACTCTCTTCTTCTTCCAGTGTGTGCTCTTCTGCTGTGGCTGGGTGGAGATAAACGCTGCTC 768
Db      733  ACTTCTCTTCTTCTTCCATCTCTGTTGTGCTGCTGGGTGAGAGATAGAGACTCTG 792
Oy      769  TTCTACAAATACATGACACAAAATACCGCACAGACAAACCGAGAAATATCATAGAG 828
Db      793  TTTTACAAAGTATGCTCTACAAAGAGTATCGAGCTGGCAAGAGAGGGGATTAATGAA 852
Oy      829  ACAGAGGGTGAACACC-----TAAGGCAATGAGATGATGGGAAATGATGAT 879
Db      853  CATGAAGAGACAGCCATCTTCTAAGACTGAATGAAATGAGCGGGAAGTGTGCTCA 912
Oy      880  TCCCATTTTCTAGATGGGAACCTGTGCTCCCTGGAAGGGAAG----- 921
Db      913  TCTCATGTGGAATTTCTTAGATGTGTGCTGCTGTGAGGTGATGAGAGGACCAA 972
Oy      922  GAAGTGTGATGATCCCGACAGAGATATCGGATTTCTCAAGATCTGAACAAAACAC 981
Db      973  GATGATGAAGAGCTAGGCGAAGAAATGGCTAAGATTTCTGAAGAACTTAAACAGAACAT 1032
Oy      982  CCAGAGAGAGACTTATGATCAGCTGTGTGAGATGCGCAATTAATGCTTTTCCACCAA 1041
Db      1033  CCAGATTAAGAAATAGAGCAATTAATAGAAATTAAGTAACCAAGCTTAAGTACAGAG 1092
Oy      1042  CAGAAAGCCGCGCTCTACCCATCCAAAGCCACTGTATGATGACTGGTGCAGGCAAT 1101
Db      1093  CAAAAGAGTGAAGCATTTTATCGCATTCAGCTACTGCTCATGACTGGAGCTGGCAAC 1152
Oy      1102  ATCTGTGAAGAAACATGACAGAGAACCCAGAGGCTTCACATGAGAGAGTGCAC 1161
Db      1153  ATTTTAAAGAGGCAATGACAGCTGACCAAGCAAGAGGCTGTGACATGACAGAGTCAAC 1212
Oy      1162  ACCGATAGCCCTG--AGACTTATTTCCAAAGCTCTCTTGAACCATGTTCTTACAG 1218
Db      1213  ACTGAATGACTGAATAATGACCCCTGTAAGTAATCTTCTTGAACAAGGACATATCAG 1272
Oy      1219  TGCTGTGAAGAACTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1278
Db      1273  TGCTGTGAAGAACTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
Oy      1279  AGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
Db      1333  AACCATGTGTTGTTGCTTCAAGACAGAGAGTGGCACAGAAATGCTGGTCTGATTAAT 1392
Oy      1339  GAGTTTCAAGAGGAGGAGGCTGTGCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1398
Db      1393  GAATTTACTGAAGAACTGTGTGTTTAAAGCTGTGTATACCCGAAGAAATAGAGTGT 1452
Oy      1399  GGCATTAATGATGACGACATTTTGGAGAGAGTGAACACTTCTTGTGAAGTTGAGCAAT 1458

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Db      1453  GGTATCATATGATGATATATCTTTGAGAGAGATGAATAATTTCTTGTGATCTCAGCAAT 1512
Oy      1459  GTCCGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1518
Db      1513  GTCAAAATATCTTGTGAAGCTGTGAAGATGGGATGCTACTGGAAGC-----CAATCAT 1563
Oy      1519  CCCTTGCTGGGCTGTGCTGAGCTCCCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1578
Db      1564  GTTCTTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1623
Oy      1579  GACCATGACGAGCATCTTCACTTGTGATGATGATGATGATGATGATGATGATGATGAT 1638
Db      1624  GACCATGACGAGCATTTTACTTGTGAGAACTGTGATGATGATGATGATGATGATGATG 1683
Oy      1639  GTTATGAGAGTCAAGTCTTCCGACATCAAGTCCCGGGGTACAGTCAATGCTCCCTT 1698
Db      1684  ATCATGAGAGTGAAGATTAAGAACTGTGAGAACTGTGAGAACTGTGAGAACTGTGAG 1743
Oy      1699  AGGACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1758
Db      1744  AAAACCATCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1803
Oy      1759  TTGGAATTCAGAAATGATGAACCTGAAA 1788
Db      1804  CTGGAATTCAGAAATGATGAATGTGTA 1833

RESULT 15
ABL09809
ID ABL09809 standard; cDNA; 4546 bp.
XX
AC ABL09809;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23909.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
PN Drosophila melanogaster.
XX
PD WO200171042-A2.
XX
PN 27-SEP-2001.
XX
PE 23-MAR-2001; 2001MO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR P-PDB; ABB65706.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 23909; 21bp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16175-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB5737-ABB72072).
CC The sequence data for this patent did not form part of the printed

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Db 2585 TACGTAGCCACTTCGTCCCTCTTTGGAGAGTTCCTTTGGCATTTGTGCCCCACT 2644
OY 2230 GAGTACGACACGAGGCTGGGCTGCGCTGCATTCCTCATATTGGCATGCTCACC 2289
Db 2645 GACATTTGGCGGCGCTATGTATTACCTTTGTGTATCCATATTCTGATTTGGCGTCATCACT 2704
OY 2290 GCCATCATTTGGGACCTGGGCTGCGCTGCGCTGACCATTTGGTCTCAAGATTCACTC 2349
Db 2705 GCCATCATTTGGGAGTGGCGCTCCTTATTTGGCTGGCGCTCAACATCAAGGACTCGTA 2764
OY 2350 ACAGCTGTCTTTCTGCGCATTTGGCACTCTGTCTCCCATATACCTTTGCCAGCAAGCT 2409
Db 2765 ACAGGCAATCCTGTGTTGGCGCTGGGCAACAGCATACATACATTCGCCAGCATGAT 2824
OY 2410 GCTGCCCTCCAGATGTAATGACAGCCCTCCATTTGGCAACGTAAGGCGAGCAAGCC 2469
Db 2825 GCCGCCAAGCATGACAGGCTGCCGATTAATTCATTCGCAATGTACGCGCAGCAATGCC 2884
OY 2470 GTCATGTCTTCTGCGCATTCGCGCTGGCTGTCTGCTGGCGCCATCTACTGGGCTCTG 2529
Db 2885 GTCAGCTGTCTCGGCGCATTCGCGCTGGCATGCGCATGGCGCGCTACACAGCTCC 2944
OY 2530 CAGGAGACAGAGTTCCAGCTGTGGCGGACACTGGCTTCTCCGTACCTCTTCAAC 2589
Db 2945 CATGGCATGTACCTCAACGTGAGGCCGGAACCATTTGATTCGCCGTGCGCTTCTGC 3004
OY 2590 ATCTTGCATTTGCTGCTCATCAGGCTGCTTGTACCGAAGGCGGC--CGACCTGGA 2646
Db 3005 GCGAGGCGCTGATTTGCCATTAATGCTCATATGTTCCGGCGTGGCACAAAGGCAATGGC 3064
OY 2647 GGGAGAGCTTGTGGCCCGCTGGCTGCGACGCTGCCAACAATGGCTCTTTGTAGGCTG 2706
Db 3065 GCGAGCTGGGCGGTCCGAAGTATGSAATGATCATCAGCGCAGGATCTGTATTCCTG 3124
OY 2707 TGCTCTCTTACATCTTGTGCACTAGAGGCTTATTGCTACATCAAGG 2758
Db 3125 TGGGTGTTCTACGTGGTTATATGATCTGTAAGCCCTACGACGTCATCCGGG 3176

Search completed: November 30, 2002, 10:20:30
Job time : 430 secs